Claims

1 through 5. (Cancelled)

6. (Previously presented) A nucleic acid molecule having a nucleic acid sequence encoding a variant cellobiohydrolase that is mutated with respect to a wild-type cellobiohydrolase of SEQ ID NO: 5, the mutation providing means for improving functionality of the variant cellobiohydrolase with respect to the wild-type cellobiohydrolase.

7. (Currently amended) The nucleic acid molecule of claim 6 wherein the means for improving is selected from the group consisting of:

(a) proline substituted at a position selected from the group consisting of position 8, 27, 43, 75, 94, 190, 195, 287, 299, 312, 315, 359, 398, 401, 414, 431, 433, and any combination thereof;

(b) a helix-capping mutation defined as an arginine or aspartic acid residue is substituted at a position selected from the group consisting of position 64, 337, 327, 405, 410 and any combination thereof;

(c) substitution of glycine at position 99;

(d) substitution of cysteine at positions 197 and 370;

(e) substitution of a non-glycosyl accepting amino acid residue in place of an N-glycosylation site amino acid residue at a position selected from the group consisting of position 45, 270, 384 and any combination thereof,

(f) alanine substitution at a position selected from the group consisting of position 45, 270, 384 and any combination thereof; and

(g) any combination of the mutations of (a), (b), (c), (d), (e), (f), wherein the positional reference is within the amino acid sequence of the wild-type cellobiohydrolase of SEQ ID NO: 5.

8. (Previously presented) The nucleic acid molecule of claim 7 wherein the means for improving comprises the proline substituted at a position selected from the group consisting of position 8, 27, 43, 75, 94, 190, 195, 287, 299, 312, 315, 359, 398, 401, 414, 431, 433, and any combination thereof.

9. (Previously presented) The nucleic acid molecule of claim 7 wherein the means for improving comprises the helix-capping mutation defined as an arginine or aspartic acid residue is substituted at a position selected from the group consisting of position 64, 337, 327, 405, 410 and any combination thereof.

10. (Currently amended) The nucleic acid molecule of claim 7 wherein the means for improving comprises substitution of glycine at position 99.

11. (Currently amended) A method for mutating a nucleic acid encoding a wild type cellobiohydrolase of SEQ ID NO: 5, the method comprising:

mutating the wild type cellobiohydrolase with a mutation selected from the group consisting of:

(a) proline substituted at a position selected from the group consisting of position 8, 27, 43, 75, 94, 190, 195, 287, 299, 312, 315, 359, 398, 401, 414, 431, 433, and any combination thereof;

(b) a helix-capping mutation defined as an arginine or aspartic acid residue is substituted at a position selected from the group consisting of position 64, 337, 327, 405, 410 and any combination thereof;

(c) substitution of glycine at position 99;

(d) substitution of cysteine at positions 197 and 370;

(e) substitution of a non-glycosyl accepting amino acid residue in place of an N-glycosylation site amino acid residue at a position selected from the group consisting of position 45, 270, 384 and any combination thereof,

(f) alanine substitution at a position selected from the group consisting of position 45, 270, 384 and any combination thereof; and

(g) any combination of the mutations of (a), (b), (c), (d), (e), (f), wherein the positional reference is within the amino acid sequence of the wild-type cellobiohydrolase of SEQ ID NO: 5.

12. (Currently amended) The method of claim 11, wherein the mutation comprises substitution of a non-glycosyl accepting amino acid residue in place of an N-glycosylation site amino acid residue at a position selected from the group consisting of position 45, 270, 384 and any combination thereof.

13. (Previously presented) The method of claims 11, wherein the step of mutating comprises site-directed mutagenesis.

14. (Currently amended) The method of claim 11, further comprising a step of shortening a linker region of the wild-type cellobiohydrolase with respect to wild-type linker region SEQ ID NO: 2 to provide a linker region having a length of from about 6 amino acids to about 17 amino acids located, between a catalytic domain and a cellulose binding domain (CBD) of SEQ ID NO: 5.

15. (Currently amended) An exoglucanase, comprising the sequence change encoded by SEQ ID NO: 71.

16. (Currently amended) An exoglucanase, comprising the sequence change encoded by SEQ ID NO: 74.

17. (Cancelled).

18. (Cancelled).

19. (Cancelled) The nucleic acid molecule of claim 7 wherein the means for enhancing thermostability comprises the a deletion of a segment of the wild-type cellobiohydrolase selected from the group consisting of position 99-101, position 278-279, and position 387, and any combination thereof.

20. (Currently amended) The nucleic acid molecule of claim 7 wherein the means for enhancing thermostability comprises substitution of a cysteine at positions 197 and 370.

21. (Currently amended) The nucleic acid molecule of claim 7 wherein the means for enhancing thermostability comprises substitution of a non-glycosyl accepting amino acid residue in place of an N-glycosylation site amino acid residue at a position selected from the group consisting of position 45, 270, 384 and any combination thereof.

22. (Currently amended) The nucleic acid molecule of claim 7 wherein the means for enhancing thermostability comprises substitution of an alanine at a position selected from the group consisting of position 45, 270, 384 and any combination thereof.

23. (Cancelled).

24. (Previously presented) The nucleic acid molecule of claim 7 wherein the means for improving comprises means for enhancing thermostability.

25. (Currently amended) The nucleic acid molecule of claim 6, wherein the variant cellobiohydrolase comprises a linker region having a length of from about 6 amino acids to about 17 amino acids located, between a catalytic domain and a cellulose binding domain (CBD).

26. (Currently amended) A nucleic acid molecule having a nucleic acid sequence encoding a variant cellobiohydrolase that is mutated with respect to a wild-type cellobiohydrolase of SEQ ID NO: 5, the mutation selected from the group consisting of:

(a) proline substituted at a position selected from the group consisting of position 8, 27, 43, 75, 94, 190, 195, 287, 299, 312, 315, 359, 398, 401, 414, 431, 433, and any combination thereof;

(b) a helix-capping mutation defined as an arginine or aspartic acid residue is substituted at a position selected from the group consisting of position 64, 337, 327, 405, 410 and any combination thereof;

(c) substitution of glycine at position 99;

(d) substitution of cysteine at positions 197 and 370;

(e) substitution of a non-glycosyl accepting amino acid residue in place of an N-glycosylation site amino acid residue at a position selected from the group consisting of position 45, 270, 384 and any combination thereof,

(f) alanine substitution at a position selected from the group consisting of position 45, 270, 384 and any combination thereof; and

(g) any combination of the mutations of (a), (b), (c), (d), (e), (f), wherein the positional reference is within the amino acid sequence of the wild-type cellobiohydrolase of SEQ ID NO: 5.

27. (New) An exoglucanase, comprising the sequence change encoded by SEQ ID NO: 77.

28. (New) An exoglucanase composition, comprising a combination of exoglucanases selected from the group consisting of exoglucanases defined by claims 15, 16 and 27.